GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:17 ; Search time 8498.8 Seconds
(without alignments)
31.610 Million cell updates/sec

Title: US-09-851-670-6
Perfect score: 25
Sequence: 1 ccctaggccccaccagtctactgct 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15.8	63.2	54	13	AZ766014	AZ766014 1M0563H17
	2	15.6	62.4	52	13	AZ327082	AZ327082 1M0050D15
	3	14.6	58.4	43	13	AZ762861	AZ762861 1M0558P04
	4	14.6	58.4	57	10	AA291683	AA291683 zt39d03.s
c	5	14.2	56.8	43	10	AI048043	AI048043 vn21f12.r
c	6	13.8	55.2	45	13	AZ599477	AZ599477 1M0414B20
	7	13.8	55.2	50	10	AU104177	AU104177 AU104177
	8	13.8	55.2	50	10	AU104182	AU104182 AU104182
	9	13.8	55.2	50	10	AU104190	AU104190 AU104190
c	10	13.6	54.4	27	13	AZ774487	AZ774487 2M0004D01
	11	13.6	54.4	56	11	BF018760	BF018760 ux97h05.x
c	12	13.4	53.6	42	13	AZ370282	AZ370282 1M0121C16
	13	13.2	52.8	28	13	AZ586097	AZ586097 1M0391G17
	14	13.2	52.8	43	11	BE896209	BE896209 601438919
	15	13	52.0	32	13	AZ581120	AZ581120 1M0369E02
c	16	12.8	51.2	40	10	AA811470	AA811470 ob83d02.s
c	17	12.8	51.2	50	10	AU102901	AU102901 AU102901
c	18	12.8	51.2	50	10	AU102902	AU102902 AU102902
c	19	12.8	51.2	50	10	AU105107	AU105107 AU105107
c	20	12.8	51.2	50	10	AU105124	AU105124 AU105124
c	21	12.8	51.2	55	10	AI150170	AI150170 qf34b07.x
	22	12.6	50.4	46	10	AA867748	AA867748 vx16a12.r
	23	12.6	50.4	50	10	AU105885	AU105885 AU105885
c	24	12.6	50.4	52	11	H14777	H14777 ym24c09.s1
c	25	12.4	49.6	34	13	AZ856611	AZ856611 2M0161P06
c	26	12.4	49.6	50	10	AU102899	AU102899 AU102899
c	27	12.4	49.6	50	10	AU102900	AU102900 AU102900
c	28	12.4	49.6	50	10	AU107387	AU107387 AU107387
c	29	12.4	49.6	50	10	AU107388	AU107388 AU107388
c	30	12.4	49.6	50	10	AU107389	AU107389 AU107389
	31	12.4	49.6	59	10	AA419276	AA419276 zv35e04.s
	32	12.4	49.6	60	10	AI984456	AI984456 wr83b02.x
c	33	12.2	48.8	21	13	AZ596843	AZ596843 1M0410C23
	34	12.2	48.8	41	13	AZ775318	AZ775318 2M0007B12
c	35	12.2	48.8	46	10	AA985334	AA985334 am79g08.s
c	36	12.2	48.8	49	10	AA011834	AA011834 mh01c08.r
	37	12.2	48.8	50	10	AU104186	AU104186 AU104186
c	38	12.2	48.8	51	13	AZ591236	AZ591236 1M0401P06
	39	12.2	48.8	52	11	H39343	H39343 DR26 IFNgam
	40	12.2	48.8	54	13	AZ576640	AZ576640 AST-TD13S
c	41	12.2	48.8	55	10	AA894695	AA894695 oj27d05.s
	42	12.2	48.8	56	13	AZ775455	AZ775455 2M0007G23
c	43	12.2	48.8	58	10	AI095308	AI095308 oy20f06.s
c	44	12.2	48.8	58	10	AI375271	AI375271 tc11c09.x
	45	12.2	48.8	60	13	AZ456310	AZ456310 1M0259M03

ALIGNMENTS

RESULT 1
AZ766014
LOCUS AZ766014 54 bp DNA GSS 16-FEB-2001
DEFINITION 1M0563H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0563H17 F, DNA sequence.
ACCESSION AZ766014
VERSION AZ766014.1 GI:12882637
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 54)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0563 row: H column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 54.
FEATURES Location/Qualifiers
source 1. .54

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                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0563H17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       11 a     16 c     13 g     14 t
ORIGIN


  Query Match             63.2%;  Score 15.8;  DB 13;  Length 54;
  Best Local Similarity   89.5%;  Pred. No. 1.2e+04;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ccctaggccccaccagtct 19
          ||| |||||| ||||||||
Db     18 CCCAAGGCCCAACCAGTCT 36


RESULT   2
AZ327082
LOCUS       AZ327082       52 bp    DNA             GSS       29-SEP-2000
DEFINITION  1M0050D15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0050D15 F, DNA sequence.
ACCESSION   AZ327082
VERSION     AZ327082.1  GI:10385476
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0050  row: D  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 52.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0050D15"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       16 a     13 c     11 g     12 t
ORIGIN


  Query Match             62.4%;  Score 15.6;  DB 13;  Length 52;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+04;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ccctaggccccaccagtctact 22
          ||| || || |||||||| |||
Db     11 CCCAAGACCACACCAGTCAACT 32


RESULT   3
AZ762861
LOCUS       AZ762861       43 bp    DNA             GSS       16-FEB-2001
DEFINITION  1M0558P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0558P04 F, DNA sequence.
ACCESSION   AZ762861
VERSION     AZ762861.1  GI:12873302
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0558  row: P  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 43.
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FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0558P04"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       12 a     15 c      8 g      8 t
ORIGIN


  Query Match             58.4%;  Score 14.6;  DB 13;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 3.6e+04;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       5 aggccccaccagtctactgct 25
           ||| |||| || ||| |||||
Db      20 AGGACCCAACATTCTGCTGCT 40


RESULT   4
AA291683
LOCUS       AA291683       57 bp    mRNA            EST       16-MAY-1997
DEFINITION  zt39d03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:724709 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE
            DEHYDROGENASE, LIVER (HUMAN);, mRNA sequence.
ACCESSION   AA291683
VERSION     AA291683.1  GI:1939679
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:724709"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT       8 a     19 c     17 g     13 t
ORIGIN


  Query Match             58.4%;  Score 14.6;  DB 10;  Length 57;
  Best Local Similarity   81.0%;  Pred. No. 3.7e+04;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 ccctaggcccccaccagtctac 21
           |||||||||||  ||  ||| |
Db       8 CCCTAGGCCCCTCCCCTCTTC 28


RESULT   5
AI048043/c
LOCUS       AI048043       43 bp    mRNA            EST       08-JUL-1998
DEFINITION  vn21f12.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA
            clone IMAGE:1021871 5' similar to WP:T13H5.2 CE03653
            RETINAL-BINDING LIKE PROTEIN ;, mRNA sequence.
ACCESSION   AI048043
VERSION     AI048043.1  GI:3296330
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:572647
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Mus musculus"
                     /strain="B6D2 F1/J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1021871"
                     /clone_lib="Knowles Solter mouse blastocyst B1"
                     /tissue_type="blastocyst"
```

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                     /dev_stage="embryo (pre-implantation)"
                     /lab_host="DH10B"
                     /note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally from mRNA prepared
                     from 800 blastocysts.   Primer: SalI(dT):
                     5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'.  cDNAs  were
                     cloned into the NotI/SalI sites of a pSPORT vector (Life
                     Technologies).  Two different size selections:  B1 (larger
                     inserts) and B3."
BASE COUNT       13 a      5 c     16 g      9 t
ORIGIN


  Query Match             56.8%;  Score 14.2;  DB 10;  Length 43;
  Best Local Similarity   84.2%;  Pred. No. 5.2e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 aggccccaccagtctactg 23
           || |||| |||| ||||||
Db      42 AGCCCCCTCCAGGCTACTG 24


RESULT   6
AZ599477/c
LOCUS       AZ599477       45 bp    DNA             GSS       13-DEC-2000
DEFINITION  1M0414B20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0414B20 R, DNA sequence.
ACCESSION   AZ599477
VERSION     AZ599477.1  GI:11721667
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0414  row: B  column: 20
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 45.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0414B20"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       13 a      5 c     16 g     11 t
ORIGIN


  Query Match             55.2%;  Score 13.8;  DB 13;  Length 45;
  Best Local Similarity   72.0%;  Pred. No. 7.5e+04;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ccctaggccccaccagtctactgct 25
           ||| | |||||||| || |  | ||
Db      29 CCCAATGCCCCACCCGTTTCTTTCT 5


RESULT   7
AU104177
LOCUS       AU104177       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU104177 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HSI04173, mRNA sequence.
ACCESSION   AU104177
VERSION     AU104177.1  GI:13553698
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HSI04173"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT       11 a      20 c      6 g     13 t
ORIGIN


  Query Match             55.2%;  Score 13.8;  DB 10;  Length 50;
  Best Local Similarity   72.0%;  Pred. No. 7.5e+04;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ccctaggccccaccagtctactgct 25
           |||  ||||| ||| |||  || ||
Db       6 CCCCTGGCCCAACCCGTCATCTACT 30


RESULT   8
AU104182
LOCUS       AU104182       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU104182 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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            KAT02326, mRNA sequence.
ACCESSION   AU104182
VERSION     AU104182.1  GI:13553703
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="KAT02326"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT       11 a     20 c      6 g     13 t
ORIGIN


  Query Match             55.2%;  Score 13.8;  DB 10;  Length 50;
  Best Local Similarity   72.0%;  Pred. No. 7.5e+04;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ccctaggccccaccagtctactgct 25
           |||  ||||| ||| |||  || ||
Db       7 CCCCTGGCCCAACCCGTCATCTACT 31


RESULT  9
AU104190
LOCUS       AU104190       50 bp    mRNA            EST       05-APR-2001
DEFINITION  AU104190 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            LNG15187, mRNA sequence.
ACCESSION   AU104190
VERSION     AU104190.1  GI:13553711
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
            ,K., Suyama,A. and Sugano,S.
  TITLE     Fine Structural analysis of transcription start sites of human
            mRNAs using full-length enriched and 5'-end enriched cDNA libraries
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="LNG15187"
                     /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT       16 a     17 c      6 g     11 t
ORIGIN


  Query Match             55.2%;  Score 13.8;  DB 10;  Length 50;
  Best Local Similarity   72.0%;  Pred. No. 7.5e+04;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ccctaggccccaccagtctactgct 25
           |||  ||||| ||| |||  || ||
Db      22 CCCCTGGCCCAACCCGTCATCTACT 46


RESULT  10
AZ774487/c
LOCUS       AZ774487       27 bp    DNA             GSS       16-FEB-2001
DEFINITION  2M0004D01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0004D01 F, DNA sequence.
ACCESSION   AZ774487
VERSION     AZ774487.1  GI:12899988
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0004  row: D  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0004D01"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
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adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 5 a 2 c 12 g 8 t
ORIGIN

Query Match 54.4%; Score 13.6; DB 13; Length 27;
Best Local Similarity 80.0%; Pred. No. 8.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 aggccccaccagtctactgc 24
|| |||||||| || | |||
Db 20 AGACCCCACCACTCAATTGC 1

RESULT 11
BF018760
LOCUS BF018760 56 bp mRNA EST 29-DEC-2000
DEFINITION ux97h05.x1 McCarrey Eddy spermatocytes Mus musculus cDNA clone
IMAGE:3656505 3', mRNA sequence.
ACCESSION BF018760
VERSION BF018760.1 GI:10750092
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 56)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: ux97h05.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1418809
Seq primer: Primer name ambiguous.
FEATURES Location/Qualifiers
source 1. .56
/organism="Mus musculus"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:3656505"
/clone_lib="McCarrey Eddy spermatocytes"
/sex="male"
/tissue_type="spermatocytes, pooled from multiple mice"
/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pBluescript SK+ (Stratagene
); Site_1: XhoI; Site_2: EcoRI; cDNA oligo dT-primed
[5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTT-3'] and directionally
cloned using 5' linkers 5'-AATTCGGCACGAG-3' and
5'-CTCGTGCCG-3'. Size selection of >400bp material gives
average insert size ranging from 1-2 kb. Library was mass
excised (from lambda-UniZAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 98% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63422."
BASE COUNT 15 a 13 c 11 g 17 t
ORIGIN

Query Match 54.4%; Score 13.6; DB 11; Length 56;
Best Local Similarity 80.0%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ccctaggccccaccagtcta 20
| || |||||||||||| | |
Db 33 CACTGGGCCCCACCAGGCAA 52

RESULT 12
AZ370282/c
LOCUS AZ370282 42 bp DNA GSS 02-OCT-2000
DEFINITION 1M0121C16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0121C16 F, DNA sequence.
ACCESSION AZ370282
VERSION AZ370282.1 GI:10483982
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 42)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0121 row: C column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 42.
FEATURES Location/Qualifiers
source 1. .42
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0121C16"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 8 a 4 c 14 g 16 t
ORIGIN

Query Match 53.6%; Score 13.4; DB 13; Length 42;
Best Local Similarity 73.9%; Pred. No. 1.1e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 ctaggccccaccagtctactgct 25
|||| | ||| || | ||||||
Db 34 CTAGCCTCCAGCATTAAACTGCT 12

RESULT 13
AZ586097
LOCUS AZ586097 28 bp DNA GSS 13-DEC-2000
DEFINITION 1M0391G17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391G17 R, DNA sequence.
ACCESSION AZ586097
VERSION AZ586097.1 GI:11708287
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: G column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
FEATURES Location/Qualifiers
source 1. .28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0391G17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 6 a 11 c 3 g 8 t
ORIGIN

Query Match 52.8%; Score 13.2; DB 13; Length 28;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 cctaggccccaccagtct 19
||| |||||||||| |||
Db 11 CCTGTGCCCCACCATTCT 28

RESULT 14
BE896209
LOCUS BE896209 43 bp mRNA EST 20-OCT-2000
DEFINITION 601438919F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923716 5', mRNA sequence.
ACCESSION BE896209
VERSION BE896209.1 GI:10360382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9760 row: f column: 05
High quality sequence stop: 43.
FEATURES Location/Qualifiers
source 1. .43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3923716"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
BASE COUNT 11 a 11 c 11 g 10 t
ORIGIN

Query Match 52.8%; Score 13.2; DB 11; Length 43;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 aggccccaccagtctact 22
||| |||||||| ||| |
Db 10 AGGTCCCACCAGGCTATT 27

RESULT 15
AZ581120
LOCUS AZ581120 32 bp DNA GSS 13-DEC-2000
DEFINITION 1M0369E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369E02 R, DNA sequence.

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ACCESSION   AZ581120
VERSION     AZ581120.1  GI:11695814
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0369  row: E  column: 02
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0369E02"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT        8 a      9 c      9 g      6 t
ORIGIN


  Query Match            52.0%;  Score 13;  DB 13;  Length 32;
  Best Local Similarity  76.2%;  Pred. No. 1.5e+05;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      5 aggccccaccagtctactgct 25
          |||||  ||| | | ||||||
Db      3 AGGCCATACCTGACAACTGCT 23


Search completed: March  9, 2002, 00:09:19
Job time: 11035 sec
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